

```
<110> Allen, Steve
      Kinney, Tony
      Miao, Gou-Hua
      Orozco, Buddy
<120>
      PLANT BIOTIN SYNTHASE
      BB1429 US NA
<130>
<140>
<141>
<150>
      60/172929
      December 21, 1999
<151>
<160> 36
<170> Microsoft Office 97
<210> 1
<211> 512
<212> DNA
<213> Hordeum vulgare
<220>
<221> unsure
<222>
      (94)
<220>
<221> unsure
<222>
      (460)
<220>
<221> unsure
<222>
      (462)
<400>
caactccctc ggcagtatcg cctagtgcag cagcggctcc gttccggcca gctttgctcg 60
ccgagccggc catgatgctg ctgctcgcgc gcancttcgc tcccgcgtcc ggtccccctt 120
cgcctccgcc gttagcgccg cgcccttctc atcggtatcg gcggccgcgg cggaggcgga 180
cgggcggtgc gggacgggcc caggaacgac tggacccgcc ccgagatcca ggccatctac 240
gactccccgc tcctcgacct cctcttccac ggggctcaag tccataggaa tgtccataaa 300
tttagagaag tgcaacaatg cacacttctt tcaataaaga ctggtgggtg cagcgaagat 360
tgttcatact gcccacagtc ttcaagatac agtaccggat tgaaggctga aaaattaatg 420
aagaaagatg ccgtcctaga agcagctaaa aaggcaaagn angctgggag cacccgattt 480
                                                                  512
tgattggagc gatggagaga gacaattggc ag
<210> 2
<211> 137
<212> PRT
<213> Hordeum vulgare
<220>
<221> UNSURE
<222> (131)
```

```
<400> 2
Met Met Leu Leu Leu Ala Arg Ser Leu Arg Ser Arg Val Arg Ser Pro
Phe Ala Ser Ala Val Ser Ala Ala Pro Phe Ser Ser Val Ser Ala Ala
             20
                                 25
Ala Ala Glu Ala Glu Arg Ala Val Arg Asp Gly Pro Arg Asn Asp Trp
Thr Arg Pro Glu Ile Gln Ala Ile Tyr Asp Ser Pro Leu Leu Asp Leu
                         55
Leu Phe His Gly Ala Gln Val His Arg Asn Val His Lys Phe Arg Glu
                                          75
Val Gln Gln Cys Thr Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu
                                      90
Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Ser Thr Gly Leu Lys
                                105
                                                     110
Ala Glu Lys Leu Met Lys Lys Asp Ala Val Leu Glu Ala Ala Lys Lys
                             120
                                                 125
Ala Lys Xaa Ala Gly Ser Thr Arg Phe
                        135
<210>
      3
<211> 496
<212> DNA
<213>
       Zea mays
<220>
<221>
       unsure
<222>
       (33)
<220>
<221>
       unsure
<222>
       (318)
<220>
<221>
       unsure
<222>
       (321)
<220>
<221>
       unsure
<222>
       (365)
<220>
<221>
       unsure
<222>
       (446)
<400>
tccaatcggg tgggcagttt ttaaggaaac canggaccgc aagcaagcaa gccgccccag 60
ccgacgaggc gaggagcgtg caattccgta gctgcaacga actccctcga ccgtatcgcc 120
cgctgctcct ctatcccttt cctgctgctg ctactacctt aagctatcac tatcatggcc 180
ttgatgctgc tagcgcgcaa cctgcgctcc cgcctccgcc caccgctcgc cgccgccgcg 240
gggttctcgt cggccgcggc ggaggcggag agggcgatac gggacgggcc gcggaacgac 300
tggagccggc ccgagatnca ngccgtctac gactcaccgc tcctcgacct cctctttcac 360
```

```
ggggntcagt catcaagata caacactgga ttgaagggcc aaaaattgat gaacaaatat 420 gctgtcttgg gagcagcaaa aaaggnaaaa gagtctggga agcaaccgtt tttgcatggg 480 aactgcattg gagaaa 496
```

```
<210>
      4
<211>
      102
<212>
      PRT
<213>
     Zea mays
<220>
<221>
      UNSURE
<222>
      (48)..(49)
<220>
<221> UNSURE
<222>
      (64)
<220>
<221> UNSURE
<222>
      (91)
```

<400> 4

Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro 1 5 10 15

Pro Leu Ala Ala Ala Gly Phe Ser Ser Ala Ala Glu Ala Glu 20 25 30

Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Xaa 35 40 45

Xaa Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Xaa 50 55 60

Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Gly Gln Lys Leu Met Asn 65 70 75 80

Lys Tyr Ala Val Leu Gly Ala Ala Lys Lys Xaa Lys Glu Ser Gly Lys 85 90 95

Gln Pro Phe Leu His Gly 100

```
<210> 5
<211> 497
<212> DNA
<213> Zea mays
<220>
<221>
      unsure
      (192)
<222>
<220>
<221>
      unsure
<222>
      (460)
<220>
<221>
      unsure
<222>
      (463)
```

```
<220>
<221>
      unsure
<222>
      (469)
<220>
<221>
      unsure
<222>
      (490)
<400>
agccgacgag gcgaggagcg tgcaattccg tagctgcaac tgcaacgaac tccctccctc 60
cctcgaccgt atcgcccgct gctcctctat ccctttcctg ctgctgctac taccttaagc 120
tatcatggcc ttgatgctgc tagcgcgcaa cctgcgctcc cgcctccgcc caccgctcgc 180
cgccgccgcg gngttctcgt cggccgcggc ggaggcggag agggcgatac gggacgggcc 240
geggaacgae tggageegge eegagattea ageegtetae gaeteaeege teetegaeet 300
cctctttcac ggggctcaag tccacagaaa tgtccataaa ttcaagagaa gtgcagcaat 360
gcacacttct ttcaatcaag actggtggga tgcagtgaag attgttctta ctgtcctcaa 420
gtcatcaaag aatacaacac tgggattgaa gggcccaaan aanttgatna acaaaagatg 480
ctgtcttggn aacaaca
<210>
       6
<211> 98
<212> PRT
<213> Zea mays
<220>
<221> UNSURE
<222>
      (23)
<220>
<221> UNSURE
<222>
      (72)
<220>
<221> UNSURE
       (89)
<222>
<400> 6
Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro
Pro Leu Ala Ala Ala Xaa Phe Ser Ser Ala Ala Ala Glu Ala Glu
             20
Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile
Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
                         55
Gln Val His Arg Asn Val His Xaa Ser Arg Glu Val Gln Gln Cys Thr
Leu Leu Ser Ile Lys Thr Gly Gly Xaa Ser Glu Asp Cys Ser Tyr Cys
Pro Gln
<210>
<211> 1152
```

<212>

DNA

```
<213>
      Zea mays
<400>
gcagccgacg aggcgaggag cgtgcaattc cgtagctgca acgaactccc tcgaccgtat
cgcccgctgc tcctctatcc ctttcctgct gctgctacta ccttaagcta tcactatcat
ggccttgatg ctgctagcgc gcaacctgcg ctcccgcctc cgcccaccgc tcgccgccgc
cgcggcgttc tcgtcggccg cggcggaggc ggagagggcg atacgggacg ggccgcggaa
cgactggagc cggcccgaga tccaggccgt ctacgactca ccgctcctcg acctcctctt
tcacggggct caggtccaca gaaatgtcca taaattcaga gaagtgcagc aatgcacact
tctttcaatc aagactggtg gatgcagtga agattgttct tactgtcctc agtcatcaag
atacaacact ggattgaagg cccaaaaatt gatgaacaaa tatgctgtct tggaagcagc
aaaaaaggca aaagagtctg ggagcacccg tttttgcatg ggagctgcat ggagagaaac
cattggcagg aaatcaaact tcaaccagat tcttgaatat gtcaaggaaa taaggggtat
gggcatggag gtctgttgca cactaggcat gatagagaaa caacaagctg aagaactcaa
gaaggotgga ottacagoat ataatoataa ootagataca toaagagagt attatoocaa
cattattacc acaagatcat atgatgatag actgcagact cttgagcatg tccgtgaagc
tggaataagc atctgctcag gtggaatcat tggtcttggt gaagcagagg aggaccgggt
agggttgttg cataccctag ctaccttgcc tacacaccca gagagcgttc ctattaatgc
attggttgct gtaaaaggca cacctcttga ggaccagaag cctgtagaga tctgggaaat
gatccgcatg atcgccactg ctcggatcac gatgccaaag gcaatggtga ggctttcagc 1020
aggeegagta eggttetega tgeeagaaca agegetgtge tteetegetg gggeeaacte 1080
catcettgee ggegagaaac tteteacaac egcaaacaac gaetttgatg eggaceaage 1140
                                                                   1152
gatgttcaag at
<210>
       344
<211>
<212>
       PRT
<213>
       Zea mays
<400>
Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro
Pro Leu Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu
Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile
Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr
Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys
                 85
Pro Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met
Asn Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly
                             120
        115
Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg
                         135
```

60

120

180 240

360

420

480 540

600

660

720

780

840 900

960

160

155

Lys Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly

<211> 119

```
Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu Lys Gln Gln
Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu
            180
                                185
Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Ser Tyr
                            200
Asp Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser
                        215
Ile Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg
                    230
                                        235
Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser
                245
                                    250
Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu Asp
Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr Ala
Arg Ile Thr Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val
                        295
Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn
                    310
Ser Ile Leu Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe
                                    330
                325
Asp Ala Asp Gln Ala Met Phe Lys
            340
<210>
      9
<211> 562
<212> DNA
<213> Argemone mexicana
<220>
<221> unsure
<222>
      (553)
<400>
cattcgagaa ataaagagct gtaaaatttt tagggttttt ctgcataact ctacactcga 60
agcttcatca atagaaatat cataaacaga agaattcaaa atgcttaaag ttcaatcttt 120
gagagetegt ettegacett tgatttteat ttetaeattt tettetetet eateatette 180
ttcttcttca gctgctgctg ttcaagcaga aagaacgatt aaagaaggtc caagaaacga 240
ttqqaqcaqa qatqaaatta aatcggttta tgattctcca gttctcgatc ttctcttcca 300
tgcagctcaa gtccatagac atgctcacaa cttcagggaa gtgcagcaat gtactcttct 360
ctctgttaag acaggtgggt gcagtgaaga ttgttcatat tgtccacaat cttccaggta 420
tgacactgga gtgaaagccc aaaagctgat gaacaaggga cgcagttctg caaggaagca 480
aqaaaaqqca aaggaggcgg ggtagtacac gttttcgcaa tggtggctgc aatggggaga 540
tacaatqqqq aangaagaac aa
<210> 10
```

```
<212> PRT
<213>
      Argemone mexicana
Met Leu Lys Val Gln Ser Leu Arg Ala Arg Leu Arg Pro Leu Ile Phe
Ile Ser Thr Phe Ser Ser Leu Ser Ser Ser Ser Ser Ser Ala Ala
                                 25
Ala Val Gln Ala Glu Arg Thr Ile Lys Glu Gly Pro Arg Asn Asp Trp
Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Val Leu Asp Leu
Leu Phe His Ala Ala Gln Val His Arg His Ala His Asn Phe Arg Glu
                                         75
Val Gln Gln Cys Thr Leu Leu Ser Val Lys Thr Gly Gly Cys Ser Glu
Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Asp Thr Gly Val Lys
Ala Gln Lys Leu Met Asn Lys
        115
<210>
       11
<211> 1340
<212> DNA
<213> Glycine max
<400>
      11
ctaqtactqc tccctctgcg acttcgtttc gtagagggat tttggccgcc aaataaacag
tctcaccata aactccaaag tcccaacgct aaacgaaacc aaaccccaaa cacaaatacc
gttgttgtct gttgtctctg tcgtgtctat attcgcagat ctctcactca ttctctgttg
tttctctgcc caacttcgaa ttcgaaagca aaaacatgtt tttggcgaga cccattttcc
gagcaccete cetttgggeg ttgcactett cetacgegta tteetetgee teagcagetg
caattcaagc tgagagagcc atcaaagaag gacccagaaa cgattggagc cgagaccaag
tcaaatccat ctacgactct cccattctcg atcttctctt ccatggggct caagttcaca
                                                                   420
gacatgctca taacttcagg gaagttcaac agtgtactct tctgtctatc aaaacaggag
ggtgcagtga agattgttcc tattgtcctc aatcctctaa gtatgataca ggagtcaaaa
                                                                    540
                                                                   600
ggccaagcct tatgaacaag gaagctgttc tccaggctgc aaagaaggca aaagaggctg
ggagcactcg cttttgtatg ggtgctgcgt ggagggatac actaggaaga aagaccaact
                                                                    660
                                                                    720
tcaaccagat ccttgaatat gtgaaagaca taagggacat gggaatggag gtttgttgca
                                                                    780
cccttggcat gctggagaaa cagcaggctg ttgaactcaa gaaggcaggt ctcactgctt
ataatcacaa tottgacact toaagggagt attatocaaa cataatcaca acaaggactt
atgatgageg tetteaaace ettgagtttg ttegggatge agggateaat gtttgttetg
gaggaattat agggcttgga gaagcagagg aggatcgtgt aggtttgtta catacattgt
caacacttcc cacccatcca gagagtgttc ctattaatgc acttgttgct gtaaagggaa 1020
cccctcttga ggatcagaag cctgttgaaa tatgggagat gattcgcatg atagcaactg 1080
cacgtatcgt aatgccaaaa gcaatggtca ggttatcagc tggcagagtt cgattctcca 1140
tgcctgagca ggcattgtgc tttcttgctg gtgcaaattc tatattcact ggtgaaaagc 1200
ttctcactac tcctaacaat gattttgatg ctgatcaact catgtttaaa gttcttggac 1260
ttctcccaaa agctccaagc ttacatgaag gtgaaactag tgtgacagaa gattataagg 1320
aagcagcttc ttctagttga
```

<210> 12 <211> 374

<212> PRT <213> Glycine max

His Ser Ser Tyr Ala Tyr Ser Ser Ala Ser Ala Ala Ile Gln Ala 20 25 30

Glu Arg Ala Ile Lys Glu Gly Pro Arg Asn Asp Trp Ser Arg Asp Gln 35 40 45

Val Lys Ser Ile Tyr Asp Ser Pro Ile Leu Asp Leu Leu Phe His Gly
50 55 60

Ala Gln Val His Arg His Ala His Asn Phe Arg Glu Val Gln Gln Cys 65 70 75 80

Thr Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr 85 90 95

Cys Pro Gln Ser Ser Lys Tyr Asp Thr Gly Val Lys Arg Pro Ser Leu 100 105 110

Met Asn Lys Glu Ala Val Leu Gln Ala Ala Lys Lys Ala Lys Glu Ala 115 120 125

Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Asp Thr Leu Gly 130 135 140

Arg Lys Thr Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg 145 150 155 160

Asp Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln 165 170 175

Gln Ala Val Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn 180 185 190

Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Thr 195 200 205

Tyr Asp Glu Arg Leu Gln Thr Leu Glu Phe Val Arg Asp Ala Gly Ile 210 215 220

Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp 225 230 235 240

Arg Val Gly Leu Leu His Thr Leu Ser Thr Leu Pro Thr His Pro Glu 245 250 255

Ser Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu 260 265 270

Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr 275 280 285

Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg 290 295 300

```
Val Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala
305
                    310
                                        315
Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr Pro Asn Asn Asp
                325
                                    330
Phe Asp Ala Asp Gln Leu Met Phe Lys Val Leu Gly Leu Leu Pro Lys
            340
                                345
Ala Pro Ser Leu His Glu Gly Glu Thr Ser Val Thr Glu Asp Tyr Lys
                            360
        355
Glu Ala Ala Ser Ser Ser
    370
<210>
      13
<211>
      479
<212>
      DNA
<213> Glycine max
<400>
      13
ggcgactctc agaacttccc tatcacgatc cctcatcctc cttcgctcca atacccctaa
actcgcacct atctcttcct ctgttcgtct tcaagttcaa aagtcgagaa actatggtac 120
cgtatcatct gttcctcctc aagctacaga aacatcaagc acatcaccta gtaaggatgt 180
ctaccaagaa gcactcaacg caactgaacc ccgcagcaat tggacaagag aagaaatcaa 240
ggcgatctat gataagccat tgatggagtt atgttggggt gctggtagtt tgcacaggaa 300
attccatata cctggggcta ttcagatgtg tacattgttg aacatcaaga cgggtggttg 360
ctcggaggga ttgttcttac tggcgcccaa tcatcccgct accaaaccgg tctcaaagcc 420
ctccaaaaat ggtcctccgt cgaatctgtc ctcgcaagcc gccccgcatc gccaaaaga 479
<210> 14
<211> 52
<212> PRT
<213> Glycine max
<400> 14
Arg Ser Asn Trp Thr Arg Glu Glu Ile Lys Ala Ile Tyr Asp Lys Pro
Leu Met Glu Leu Cys Trp Gly Ala Gly Ser Leu His Arg Lys Phe His
             20
Ile Pro Gly Ala Ile Gln Met Cys Thr Leu Leu Asn Ile Lys Thr Gly
                             40
Gly Cys Ser Glu
     50
<210> 15
<211> 589
<212> DNA
<213> Triticum aestivum
<220>
<221> unsure
<222> (321)
```

```
<220>
<221> unsure
<222>
      (332)
<220>
<221> unsure
<222> (335)..(336)
<220>
<221>
     unsure
<222>
      (403)
<220>
<221> unsure
<222>
      (407)
<220>
<221> unsure
<222> (516)
<220>
<221> unsure
<222> (539)
<220>
<221> unsure
<222> (547)
<220>
<221> unsure
<222> (550)
<220>
<221> unsure
<222>
      (555)
<220>
<221> unsure
<222>
      (566)
<220>
<221> unsure
<222>
      (577)..(578)
agatgccgtc ctagaagcag caaaaaaggc aaaggaggct gggagcaccc gattttgcat 60
gggagccgca tggagagaga caattggcag gaaaacaaat ttcaaccaga ttcttgaata 120
tgtcaaggac ataagaggta tgggcatgga ggtctgttgc accctgggca tgctagagaa 180
acaacaagct gaagaactcc aagaaggctg gactttacag cttataatca taacctaaga 240
tacatccaag agaatattac ccccaacatt tattcctaca agattccgtt accgatggat 300
tagatttacc ageteette nageatgtee entinnaage tgggaattaa geegteetgg 360
tcccaaggtg ggaatttatt gggccctttg ggagaaggcc ggnaggnaaa cccgtttttt 420
aggctggttt gccatacact gggccacttt tttgcccaac acaccccaag agagcgttcc 480
cctatccaat gcatttgatt gccctgtcca agggancctc ccttccaagg ttttaaaanc 540
cctgttnaan atatnggaaa ttattnccgc atgattnncc aacccacgg
<210> 16
<211> 78
<212> PRT
<213> Triticum aestivum
```

```
<220>
<221>
      UNSURE
<222>
      (69)
<400>
Asp Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ala Gly Ser Thr
Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg Lys Thr
                                25
Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg Gly Met Gly
Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln Gln Ala Glu
Glu Leu Gln Glu Xaa Asp Phe Thr Ala Tyr Asn His Asn Leu
                    70
<210> 17
<211> 1396
<212> DNA
<213> Hordeum vulgare
<400> 17
gcaccacaac teceteggea gtategeeta gtgcageage ggeteegtte eggeeagett
tgctcgccga gccggccatg atgctgctgc tcgcgcgcag ccttcgctcc cgcgtccggt
                                                                 120
ccccttcgc ctccgccgtt agcgccgcgc ccttctcatc ggtatcggcg gccgcggcgg
                                                                 240
aggcqqagcg ggcggtgcgg gacgggccca ggaacgactg gacccgcccc gagatccagg
                                                                 300
ccatctacga ctccccgctc ctcgacctcc tcttccacgg ggctcaagtc cataggaatg
tccataaatt tagagaagtg caacaatgca cacttctttc aataaagact ggtgggtgca
gcgaagattg ttcatactgc ccacagtctt caagatacag taccggattg aaggctgaaa
aattaatgaa gaaagatgcc gtcctagaag cagctaaaaa ggcaaaggag gctgggagca
cccgattttg catgggagcc gcatggagag agacaattgg caggaaaaca aacttcaacc
agattettga atatgteaag gacataagag gtatgggeat ggaggtetgt tgeaccetgg
                                                                 600
gcatgctaga gaaacagcaa gctgaagaac tcaagaaggc tggacttaca gcttataatc
ataacctaga tacatcaaga gaatattacc cgaacattat ttctacaaga tcgtatgatg
atagattaca gactetteag catgteegtg aagetggaat aagegtetge teaggtggaa
ttattggtct tggagaggcg gaggaagacc gtgtagggct gttgcataca ctggccactt
tgccaacaca cccagagagt gttcctatca atgcattgat tgctgtcaaa ggcacgcctc
ttcaggatca gaagcctgta gagatatggg aaatgatccg catgattgcc agcgctcgga
ttgtgatgcc aaaggcaatg gtgagacttt cggcagggcg agtacggttc tccatgccag 1020
agcaagctct ctgctttctt gctggggcca actcgatctt cgccggtgaa aagctcctga 1080
caactgcaaa caacgacttt gatgcggacc aggcaatgtt caagatcctt ggcctgattc 1140
ccaaggcacc gaactttggc gatgaggagg ccaccgtggc atcatccacg gagagatgtg 1200
agcaagccgc ttcgatgtaa aatgttggta tagattctcg agaccacatc cggtgcaaaa 1260
ctggcaccat tatctccagc tagagetttg tactgtaggg atcatgatat tttgtactcc 1320
aaaaaaaaa aaaaaa
<210> 18
<211> 405
<212> PRT
<213> Hordeum vulgare
<400> 18
Thr Thr Pro Ser Ala Val Ser Pro Ser Ala Ala Ala Pro Phe
                                                        15
                                    10
```

- Arg Pro Ala Leu Leu Ala Glu Pro Ala Met Met Leu Leu Leu Ala Arg 20 25 30
- Ser Leu Arg Ser Arg Val Arg Ser Pro Phe Ala Ser Ala Val Ser Ala 35 40 45
- Ala Pro Phe Ser Ser Val Ser Ala Ala Ala Ala Glu Ala Glu Arg Ala 50 55 60
- Val Arg Asp Gly Pro Arg Asn Asp Trp Thr Arg Pro Glu Ile Gln Ala 65 70 75 80
- Ile Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala Gln Val 85 90 95
- His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr Leu Leu 100 105 110
- Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys Pro Gln 115 120 125
- Ser Ser Arg Tyr Ser Thr Gly Leu Lys Ala Glu Lys Leu Met Lys Lys 130 135 140
- Asp Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ala Gly Ser Thr 145 150 155 160
- Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg Lys Thr 165 170 175
- Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg Gly Met Gly
 180 185 190
- Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln Gln Ala Glu 195 200 205
- Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr 210 215 220
- Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Ser Thr Arg Ser Tyr Asp Asp 225 230 235 240
- Arg Leu Gln Thr Leu Gln His Val Arg Glu Ala Gly Ile Ser Val Cys 245 250 255
- Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg Val Gly 260 265 270
- Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser Val Pro 275 280 285
- Ile Asn Ala Leu Ile Ala Val Lys Gly Thr Pro Leu Gln Asp Gln Lys 290 295 300
- Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Ser Ala Arg Ile 305 310 315 320
- Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val Arg Phe 325 330 335

```
Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn Ser Ile
            340
Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe Asp Ala
                            360
Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala Pro Asn
                        375
Phe Gly Asp Glu Glu Ala Thr Val Ala Ser Ser Thr Glu Arg Cys Glu
                                                            400
385
                    390
                                        395
Gln Ala Ala Ser Met
<210> 19
<211> 1467
<212> DNA
<213> Zea mays
<400> 19
gcacgagtcc aatcgggtgg cagtttttaa ggaaaccagg gaccgcagca gcaagccgcc
ccagccgacg aggcgaggag cgtgcaattc cgtagctgca acgaactccc tcgaccgtat
                                                                    120
cgcccgctgc tcctctatcc ctttcctgct gctgctacta ccttaagcta tcactatcat
                                                                    180
ggccttgatg ctgctagcgc gcaacctgcg ctcccgcctc cgcccaccgc tcgccgccgc
cgcggcgttc tcgtcggccg cggcggaggc ggagagggcg atacgggacg ggccgcggaa
cqactqqaqc cggcccgaga tccaggccgt ctacgactca ccgctcctcg acctcctctt
tcacggggct cagtcatcaa gatacaacac tggattgaag gcccaaaaat tgatgaacaa
atatgctgtc ttggaagcag caaaaaaggc aaaagagtct gggagcaccc gtttttgcat
gggagctgca tggagagaaa ccattggcag gaaatcaaac ttcaaccaga ttcttgaata
tgtcaaggaa ataaggggta tgggcatgga ggtctgttgc acactaggca tgatagagaa
acaacaagct gaagaactca agaaggctgg acttacagca tataatcata acctagatac
atcaagagag tattatccca acattattac cacaagatca tatgatgata gactgcagac
tcttgagcat gtccgtgaag ctggaataag catctgctca ggtggaatca ttggtcttgg
                                                                    840
tgaagcagag gaggaccggg tagggttgtt gcatacccta gctaccttgc ctacacaccc
agagagcgtt cctattaatg cattggttgc tgtaaaaggc acacctcttg aggaccagaa
gcctgtagag atctgggaaa tgatccgcat gatcgccact gctcggatca cgatgccaaa
ggcaatggtg aggctttcag caggccgagt acggttctcg atgccagaac aagcgctgtg 1020
cttcctcgct ggggccaact ccatctttgc cggcgagaaa cttctcacaa ccgcaaacaa 1080
cgactttgat gcggaccagg cgatgttcaa gatccttggc ctgatcccca aggctccaag 1140
ctttggcgag gaagaggcgt ctgcggcggc tcccacagaa tccgagaggt ctgagcaagc 1200
tgcttcgatg tagaatatat acatatcatt accgattatc cgtatcacgg ttggggcgaa 1260
actagaacta ccgttgtagc tagagcattg gattgtagaa accacaacat ttcattattt 1320
tgtaattgct tgagactgaa tgggggatac ccatgtcggg ctagatcaat ggacaacttc 1380
cacacaacca aatccaaaca ttgaaactca tttttcatca cagttttaat aaacttctcc 1440
cacttatctt aaaaaaaaa aaaaaaa
<210> 20
<211> 344
<212> PRT
<213> Zea mays
<400> 20
Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro
                                                          15
  1
```

Pro Leu Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu 25

- Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile 35 40 45
- Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala 50 55 60
- Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met Asn 65 70 75 80
- Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly Ser 85 90 95
- Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg Lys
 100 105 110
- Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly Met 115 120 125
- Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu Lys Gln Gln Ala 130 135 140
- Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp 145 150 155 160
- Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Ser Tyr Asp 165 170 175
- Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser Ile 180 185 190
- Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg Val 195 200 205
- Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser Val 210 215 220
- Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu Asp Gln 225 230 235 240
- Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr Ala Arg 245 250 255
- Ile Thr Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val Arg 260 265 270
- Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn Ser 275 280 285
- Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe Asp 290 295 300
- Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala Pro 305 310 315 320
- Ser Phe Gly Glu Glu Glu Ala Ser Ala Ala Ala Pro Thr Glu Ser Glu

Arg Ser Glu Gln Ala Ala Ser Met

```
<210> 21
<211> 1515
<212> DNA
<213> Zea mays
<400> 21
ggccccagcc gacgaggcga ggagcgtgca attccgtagc tgcaactgca acgaactccc
tecetecete gaccgtateg eccgetgete etetatecet tteetgetge tgetactace
ttaagctatc atggccttga tgctgctagc gcgcaacctg cgctcccgcc tccgcccacc
gctcgccgcc gccgcggcgt tctcgtcggc cgcggcggag gcggagaggg cgatacggga
cgggccgcgg aacgactgga gccggcccga gatccaggcc gtctacgact caccgctcct
cgacctcctc tttcacgggg ctcaggtcca cagaaatgtc cataaattca gagaagtgca
gcaatgcaca cttctttcaa tcaagactgg tggatgcagt gaagattgtt cttactgtcc
tcagtcatca agatacaaca ctggattgaa ggcccaaaaa ttgatgaaca aagatgctgt
cttggaagca gcaaaaaagg caaaagagtc tgggagcacc cgtttttgca tgggagctgc
atggagagaa accattggca ggaaatcaaa cttcaaccag attcttgaat atgtcaagga
aataaggggt atgggcatgg aggtctgttg cacactaggc atgatagaga aacaacaagc
tgaagaactc aagaaggctg gacttacagc atataatcat aacctagata catcaagaga
gtattatccc aacattatta ccacaagatc atatgatgat agactgcaga ctcttgagca
tgtccgtgaa gctggaataa gcatctgctc aggtggaatc attggtcttg gtgaagcaga
ggaggaccgg gtagggttgt tgcataccct agctaccttg cctacacacc cagagagcgt
tcctattaat gcattggttg ctgtaaaagg cacacctctt gaggaccaga agcctgtaga
gatctgggaa atgatccgca tgatcgccac tgctcggatc acgatgccaa aggcaatggt 1020
gaggetttea geaggeegag taeggttete gatgeeagaa eaagegetgt getteetege 1080
tggggccaac tccatctttg ccggcgagaa acttctcaca accgcaaaca acgactttga 1140
tgcggaccag gcgatgttca agatccttgg cctgatcccc aaggctccaa gctttggcga 1200
ggaagaggtg tetgeggegg etecegeaga ateegagagg tetgageaag etgettegat 1260
gtagaatata tacatatcat taccgattat ccgtatcacg gttggggcga aactagaact 1320
acceptigtag ctagageatt ggattgtaga aaccacaaca titcattatt tigtaattgc 1380
ttgagactga atgggggata cccatgtcgg gctagatcaa aaaaaaaaa aaaaaaaaa 1440
aaaaaaaaa aaaaa
<210> 22
<211> 377
<212> PRT
<213> Zea mays
<400> 22
Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro
Pro Leu Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu
             20
Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile
Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr
Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys
                 85
Pro Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met
                                105
                                                   110
```

120

180

240

300

360

420

480 540

600 660

720

780

840

900

960

1515

Asn	Lys	Asp 115	Ala	Val	Leu	Glu	Ala 120	Ala	Lys	Lys	Ala	Lys 125	Glu	Ser	Gly	
Ser	Thr 130	Arg	Phe	Cys	Met	Gly 135	Ala	Ala	Trp	Arg	Glu 140	Thr	Ile	Gly	Arg	
Lys 145	Ser	Asn	Phe	Asn	Gln 150	Ile	Leu	Glu	Tyr	Val 155	Lys	Glu	Ile	Arg	Gly 160	
Met	Gly	Met	Glu	Val 165	Cys	Cys	Thr	Leu	Gly 170	Met	Ile	Glu	Lys	Gln 175	Gln	
Ala	Glu	Glu	Leu 180	Lys	Lys	Ala	Gly	Leu 185	Thr	Ala	Tyr	Asn	His 190	Asn	Leu	
Asp	Thr	Ser 195	Arg	Glu	Tyr	Tyr	Pro 200	Asn	Ile	Ile	Thr	Thr 205	Arg	Ser	Tyr	
Asp	Asp 210	Arg	Leu	Gln	Thr	Leu 215	Glu	His	Val	Arg	Glu 220	Ala	Gly	Ile	Ser	
Ile 225	Cys	Ser	Gly	Gly	Ile 230	Ile	Gly	Leu	Gly	Glu 235	Ala	Glu	Glu	Asp	Arg 240	
Val	Gly	Leu	Leu	His 245	Thr	Leu	Ala	Thr	Leu 250	Pro	Thr	His	Pro	Glu 255	Ser	
Val	Pro	Ile	Asn 260	Ala	Leu	Val	Ala	Val 265	Lys	Gly	Thr	Pro	Leu 270	Glu	Asp	
Gln	Lys	Pro 275	Val	Glu	Ile	Trp	Glu 280	Met	Ile	Arg	Met	Ile 285	Ala	Thr	Ala	
Arg	Ile 290	Thr	Met	Pro	Lys	Ala 295	Met	Val	Arg	Leu	Ser 300	Ala	Gly	Arg	Val	
Arg 305	Phe	Ser	Met	Pro	Glu 310	Gln	Ala	Leu	Cys	Phe 315	Leu	Ala	Gly	Ala	Asn 320	
Ser	Ile	Phe	Ala	Gly 325	Glu	Lys	Leu	Leu	Thr 330	Thr	Ala	Asn	Asn	Asp 335	Phe	
Asp	Ala	Asp	Gln 340	Ala	Met	Phe	Lys	Ile 345	Leu	Gly	Leu	Ile	Pro 350	Lys	Ala	
Pro	Ser	Phe 355	Gly	Glu	Glu	Glu	Val 360		Ala	Ala	Ala	Pro 365	Ala	Glu	Ser	
Glu	Arg 370	Ser	Glu	Gln	Ala	Ala 375	Ser	Met								
<210> 23 <211> 1439 <212> DNA <213> Zea mays																
<400> 23 gcacgagggc gaggagcgtg caattccgta gctgcaacga cgctgctcct ctatcccttt cctgctgctg ctactacctt ttgatgctgc tagcgcgcaa cctgcgctcc cgcctccgcc											aag	aagctatcac tatcatggcc				60 120 180

```
gcgttctcgt cggccgcggc ggaggcggag agggcgatac gggacgggcc gcggaacgac
                                                                   240
tggagccggc ccgagatcca ggccgtctac gactcaccgc tcctcgacct cctctttcac
                                                                   300
                                                                   360
ggggctcagg tccacagaaa tgtccataaa ttcagagaag tgcagcaatg cacacttctt
tcaatcaaga ctggtggatg cagtgaagat tgttcttact gtcctcagtc atcaagatac
                                                                   420
aacactggat tgaaggccca aaaattgatg aacaaatatg ctgtcttgga agcagcaaaa
aaggcaaaag agtctgggag cacccgtttt tgcatgggag ctgcatggag agaaaccatt
ggcaggaaat caaacttcaa ccagattctt gaatatgtca aggaaataag gggtatgggc
                                                                   600
                                                                   660
atggaggtet gttgcacaet aggeatgata gagaaacaae aagetgaaga aeteaagaag
                                                                   720
qctqqactta cagcatataa tcataaccta gatacatcaa gagagtatta tcccaacatt
attaccacaa gatcatatga tgatagactg cagactcttg agcatgtccg tgaagctgga
                                                                   780
ataagcatct gctcaggtgg aatcattggt cttggtgaag cagaggagga ccgggtaggg
                                                                   840
ttgttgcata ccctagctac cttgcctaca cacccagaga gcgttcctat taatgcattg
                                                                   900
                                                                   960
qttqctqtaa aaggcacacc tcttgaggac cagaagcctg tagagatctg ggaaatgatc
cgcatgatcg ccactgctcg gatcacgatg ccaaaggcaa tggtgaggct ttcagcaggc 1020
cgagtacggt tctcgatgcc agaacaagcg ctgtgcttcc tcgctggggc caactccatc 1080
tttqccqqcq aqaaacttct cacaaccgca aacaacgact ttgatgcgga ccaggcgatg 1140
ttcaagatcc ttggcctgat ccccaaggct ccaagctttg gcgaggaaga ggcgtctgcg 1200
geggetecca cagaateega gaggtetgag caagetgett egatgtagaa tatatacata 1260
tcattaccga ttatccgtat cacggttggg gcgaaactag aactaccgtt gtagctagag 1320
cattggattg tagaaaccac aacatttcat tattttgtaa ttgcttgaga ctgaatgggg 1380
gatacccatg tegggetaga teaatggaca acttecacae aaaaaaaaa aaaaaaaa 1439
```

<210> 24 <211> 377 <212> PRT

<213> Zea mays

<400> 24

Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro 1 5 10 15

Pro Leu Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu 20 25 30

Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile 35 40 45

Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala 50 55 60

Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr 65 70 75 80

Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys 85 90 95

Pro Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met 100 105 110

Asn Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly 115 120 125

Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg 130 135 140

Lys Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly
145 150 155 160

Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu Lys Gln Gln 165 170 175

```
Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu
Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Ser Tyr
                                                205
                            200
Asp Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser
Ile Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg
                                        235
Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser
Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu Asp
Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr Ala
                            280
Arg Ile Thr Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val
    290
                        295
Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn
                    310
                                        315
Ser Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe
                325
                                    330
Asp Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala
                                345
Pro Ser Phe Gly Glu Glu Glu Ala Ser Ala Ala Pro Thr Glu Ser
                            360
Glu Arg Ser Glu Gln Ala Ala Ser Met
                        375
    370
<210> 25
<211> 1477
<212> DNA
<213> Argemone mexicana
<400> 25
gcacgagcat tcgagaaata aagagctgta aaatttttag ggtttttctg cataactcta
                                                                     60
cactcgaagc ttcatcaata gaaatatcat aaacagaaga attcaaaatg cttaaagttc
                                                                    120
aatctttgag agctcgtctt cgacctttga ttttcatttc tacattttct tctctctcat
                                                                    180
catcttcttc ttcttcagct gctgctgttc aagcagaaag aacgattaaa gaaggtccaa
                                                                    240
gaaacgattg gagcagagat gaaattaaat cggtttatga ttctccagtt ctcgatcttc
                                                                    300
                                                                    360
tcttccatgc agctcaagtc catagacatg ctcacaactt cagggaagtg cagcaatgta
ctcttctctc tgttaagaca ggtgggtgca gtgaagattg ttcatattgt ccacaatctt
                                                                    420
ccaggtatga cactggagtg aaagcccaaa agctgatgaa caaggacgca gttctgcagg
cagcagaaaa ggcaaaggag gcgggtagta cacgtttctg catgggtgct gcatggagag
atacagtggg caggaagacc aacttcaaac agatcctcga atatgtaaaa gaaattcggg
gtatgggaat ggaggtatgc tgcactttag gcatgatcga gaagcagcaa gctgtggaac
tcaagcaggc tgggctcaca gcttacaatc ataatcttga tacttcaaga gagtattacc
ctaacatcat caccacaaga tcttacgatg agcgcttgga aactcttcag ttcgtccggg
aaqcaqggat caatgtctgc tcaggaggaa taatagggct aggagaagca gaggaggatc
```

<210> 26

<211> 379

<212> PRT

<213> Argemone mexicana

<400> 26

Met Leu Lys Val Gln Ser Leu Arg Ala Arg Leu Arg Pro Leu Ile Phe 1 5 10 15

Ile Ser Thr Phe Ser Ser Leu Ser Ser Ser Ser Ser Ser Ser Ala Ala
20 25 30

Ala Val Gln Ala Glu Arg Thr Ile Lys Glu Gly Pro Arg Asn Asp Trp
35 40 45

Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Val Leu Asp Leu 50 55 60

Leu Phe His Ala Ala Gln Val His Arg His Ala His Asn Phe Arg Glu 65 70 75 80

Val Gln Gln Cys Thr Leu Leu Ser Val Lys Thr Gly Gly Cys Ser Glu 85 90 95

Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Asp Thr Gly Val Lys 100 105 110

Ala Gln Lys Leu Met Asn Lys Asp Ala Val Leu Gln Ala Ala Glu Lys 115 120 125

Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg 130 135 140

Asp Thr Val Gly Arg Lys Thr Asn Phe Lys Gln Ile Leu Glu Tyr Val 145 150 155 160

Lys Glu Ile Arg Gly Met Gly Met Glu Val Cys Cys Thr Leu Gly Met 165 170 175

Ile Glu Lys Gln Gln Ala Val Glu Leu Lys Gln Ala Gly Leu Thr Ala 180 185 190

Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile 195 200 205

Thr Thr Arg Ser Tyr Asp Glu Arg Leu Glu Thr Leu Gln Phe Val Arg 210 215 220

```
Glu Ala Gly Ile Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu
225
                    230
Ala Glu Glu Asp Arg Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro
                245
                                    250
Ser His Pro Glu Ser Val Pro Ile Asn Ala Leu Leu Ala Val Lys Gly
            260
                                265
Thr Pro Leu Glu Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg
                            280
Met Ile Ala Thr Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu
                        295
    290
Ser Ala Gly Arg Val Arg Phe Ser Met Ser Glu Gln Ala Leu Cys Phe
Leu Ala Gly Ala Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr
                325
Pro Asn Asn Asp Phe Asp Ala Asp Gln Met Met Phe Lys Ile Leu Gly
                                345
Leu Thr Pro Lys Ala Pro Asn Phe Asp Gln Thr Ser Thr Ser Phe Glu
        355
                            360
Ala Glu Arg Cys Glu Gln Glu Ala Thr Ala Ser
                        375
    370
<210> 27
<211> 1526
<212> DNA
<213> Glycine max
<400> 27
gcacgagcta gtactgctcc ctctgcgact tcgtttcgta gagggatttt ggccgccaaa
                                                                     60
taaacagtct caccataaac tccaaagtcc caacgctaaa cgaaaccaaa ccccaaacac
                                                                    120
aaataccgtt gttgtctgtt gtctctgtcg tgtctatatt cgcagatctc tcactcattc
                                                                    180
tctgttgttt ctctgcccaa cttcgaattc gaaagcaaaa acatgttttt ggcgagaccc
attttccgag caccctccct ttgggcgttg cactcttcct acgcgtattc ctctgcctca
                                                                    360
gcagctgcaa ttcaagctga gagagccatc aaagaaggac ccagaaacga ttggagccga
qaccaaqtca aatccatcta cgactctccc attctcgatc ttctcttcca tggggctcaa
                                                                    420
gttcacagac atgctcataa cttcagggaa gttcagcagt gtactcttct gtctatcaaa
                                                                    480
acaggagggt gcagtgaaga ttgttcctat tgtcctcaat cctctaagta tgatacagga
                                                                    540
gtcaaaggcc aacgccttat gaacaaggaa gctgttctac aggctgcaaa gaaggcaaaa
                                                                    600
gaggctggga gcactcgctt ttgtatgggt gctgcatgga gggatacact gggaagaaag
                                                                    660
                                                                    720
accaacttca accagatect tgaatatgtg aaagacataa gggacatggg aatggaggtt
                                                                    780
tgttgcaccc ttggcatgct ggagaaacag caggctgttg aactcaagaa ggcaggtctc
                                                                    840
actgcctata atcacaatct tgacacttca agggagtatt atccaaacat catcacaaca
aggacttatg atgagegtet teaaaceett gagtttgtte gtgatgeagg gateaatgtt
tgttctggag gaattatagg gcttggagaa gcagaggagg atcgtgtagg tttgttacat
acattgtcaa cacttcccac ccatccagag agtgttccta ttaatgcact tgttgctgta 1020
aagggaaccc ctcttgagga tcagaagcct gttgaaatat gggagatgat tcgcatgata 1080
gcaactgcac gtatcgtaat gccaaaagca atggtcaggt tatcagctgg cagagttcga 1140
ttctccatgc ctgagcaggc attgtgcttt cttgctggtg caaattctat attcactggt 1200
gaaaagcttc tcactactcc taacaatgat tttgatgctg atcaactcat gtttaaagtt 1260
cttggacttc tcccaaaagc tccaagctta catgaaggtg aaactagtgt gacagaagat 1320
tataaqqaaq caqcttcttc tagttgagtt gtcaacggtt tcaaaacaat atctgtgatc 1380
```

cttcaacttc tctaattgct cattagcatg tactgatgtt aggtttcatt gaatttgtct 1440

aatctcagct ttgaagacac aaactccaac acttaaaaat aaatattgaa attattgatt 1500 tttccctaaa aaaaaaaaa aaaaaa 1526

<210> 28

<211> 415

<212> PRT

<213> Glycine max

<400> 28

Thr Lys Pro Asn Pro Lys His Lys Tyr Arg Cys Cys Leu Leu Ser Leu 1 5 10 15

Ser Cys Leu Tyr Ser Gln Ile Ser His Ser Phe Ser Val Val Ser Leu 20 25 30

Pro Asn Phe Glu Phe Glu Ser Lys Asn Met Phe Leu Ala Arg Pro Ile 35 40 45

Phe Arg Ala Pro Ser Leu Trp Ala Leu His Ser Ser Tyr Ala Tyr Ser 50 55 60

Ser Ala Ser Ala Ala Ala Ile Gln Ala Glu Arg Ala Ile Lys Glu Gly 65 70 75 80

Pro Arg Asn Asp Trp Ser Arg Asp Gln Val Lys Ser Ile Tyr Asp Ser 85 90 95

Pro Ile Leu Asp Leu Leu Phe His Gly Ala Gln Val His Arg His Ala 100 105 110

His Asn Phe Arg Glu Val Gln Gln Cys Thr Leu Leu Ser Ile Lys Thr 115 120 125

Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys Pro Gln Ser Ser Lys Tyr 130 135 140

Asp Thr Gly Val Lys Gly Gln Arg Leu Met Asn Lys Glu Ala Val Leu 145 150 155 160

Gln Ala Ala Lys Lys Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met 165 170 175

Gly Ala Ala Trp Arg Asp Thr Leu Gly Arg Lys Thr Asn Phe Asn Gln 180 185 190

Ile Leu Glu Tyr Val Lys Asp Ile Arg Asp Met Gly Met Glu Val Cys
195 200 205

Cys Thr Leu Gly Met Leu Glu Lys Gln Gln Ala Val Glu Leu Lys Lys 210 215 220

Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr 225 230 235 240

Tyr Pro Asn Ile Ile Thr Thr Arg Thr Tyr Asp Glu Arg Leu Gln Thr 245 250 255

Leu Glu Phe Val Arg Asp Ala Gly Ile Asn Val Cys Ser Gly Gly Ile 260 265 270

```
Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg Val Gly Leu Leu His Thr
                            280
Leu Ser Thr Leu Pro Thr His Pro Glu Ser Val Pro Ile Asn Ala Leu
                        295
Val Ala Val Lys Gly Thr Pro Leu Glu Asp Gln Lys Pro Val Glu Ile
                                        315
                    310
Trp Glu Met Ile Arg Met Ile Ala Thr Ala Arg Ile Val Met Pro Lys
                                    330
Ala Met Val Arg Leu Ser Ala Gly Arg Val Arg Phe Ser Met Pro Glu
Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn Ser Ile Phe Thr Gly Glu
Lys Leu Leu Thr Thr Pro Asn Asn Asp Phe Asp Ala Asp Gln Leu Met
                        375
    370
Phe Lys Val Leu Gly Leu Leu Pro Lys Ala Pro Ser Leu His Glu Gly
                    390
                                        395
Glu Thr Ser Val Thr Glu Asp Tyr Lys Glu Ala Ala Ser Ser Ser
                405
                                    410
<210> 29
<211> 1659
<212> DNA
<213> Glycine max
<400> 29
aaagagtgta tacagataga tttccaaact ccactcactc accactatgg cgactctcag
aacttcccta tcacgatccc tcatcctcct tcgctccaat acccctaaac tcgcacctat
                                                                    120
ctcttcctct gttcgtcttc aagttcaaaa gtcgagaaac tatggtaccg tatcatctgt
tcctcctcaa gctacagaaa catcaagcac atcacctagt aaggatgtct accaagaagc
actcaacgca actgaacccc gcagcaattg gacaagagaa gaaatcaagg cgatctatga
taagccattg atggagttat gttggggtgc tggtagtttg cacaggaaat tccatatacc
tggggctatt cagatgtgta cattgttgaa catcaagacg ggtggttgct cggaggattg
                                                                   420
ttcttactgc gcccaatcat cccgctacca aaccggtctc aaagcctcca aaatggtctc
cgtcgaatct gtcctcgcag ccgcccgcat cgccaaagac aacggtagta cacgtttctg
                                                                   540
catgggagec gegtggegeg atatgegtgg acgaaaaace aateteaaaa atgteaaaac
                                                                    600
aatggttagc gagattcgcg gaatgggtat ggaagtatgt gtcacgcttg gtatgattga
                                                                    660
tgcagagcaa gctcaggaac tcaaagaagc cggtctcacg gcttataatc ataatgtgga
                                                                   720
tacgtcgagg gatttctatc ccaaggttat cacgaccagg acttatgatg agagattgga
taccattaag aatgtgagag aggccggaat caatgtttgt acgggtggaa tcctcggatt
aggagaaaat aagtctgacc atattggact tttggagacg gttgctacgt tgccttcgca
tccggaatca tttcctgtga acatgttagt ggctatcaaa ggaacaccac tggaaggaaa
caagaaggtg gaatttgaga atatgttgag aatggttgcg acggctagaa tcgtcatgcc 1020
taaaaccatc gtgcgtttgg cagctggaag aggagaattg agcgaggaac aacaggtctt 1080
atgtttcatg gccggagcca atgccgtttt cacaggagaa acaatgttaa ccacaccagc 1140
cgttggatgg ggtgtcgatt ccgtcgtttt caacagatgg ggattaagac ccatggaaag 1200
tttcgaggtt gaagccttga agaacgataa acctgccact actaatacgg aaataccggt 1260
agaggcaagt aaggcagaga tgccaggtac agttgcttga ttgattgttt gatttggata 1320
cccagggcgt ttggtgcgct catcatctcg agtttttgca aggagattcg aacagtggaa 1380
gtgccgttgc gccaccattg ggattggcgt atcggactga gattgactgt gccacgaaaa 1440
tgttttgcgc tatcgtgtgt tgtcatctcg tgggaattta gcgttgtttg ttttgttttt 1500
```

ggttttgttt gatgtgagag aatgattgtt tagaagggga gaatgtatat acggaacagt 1560

<210> 30 <211> 417

<212> PRT

<213> Glycine max

<400> 30

Met Ala Thr Leu Arg Thr Ser Leu Ser Arg Ser Leu Ile Leu Leu Arg 1 5 10 15

Ser Asn Thr Pro Lys Leu Ala Pro Ile Ser Ser Ser Val Arg Leu Gln
20 25 30

Val Gln Lys Ser Arg Asn Tyr Gly Thr Val Ser Ser Val Pro Pro Gln 35 40 45

Ala Thr Glu Thr Ser Ser Thr Ser Pro Ser Lys Asp Val Tyr Gln Glu
50 60

Ala Leu Asn Ala Thr Glu Pro Arg Ser Asn Trp Thr Arg Glu Glu Ile 65 70 75 80

Lys Ala Ile Tyr Asp Lys Pro Leu Met Glu Leu Cys Trp Gly Ala Gly 85 90 95

Ser Leu His Arg Lys Phe His Ile Pro Gly Ala Ile Gln Met Cys Thr 100 105 110

Leu Leu Asn Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys 115 120 125

Ala Gln Ser Ser Arg Tyr Gln Thr Gly Leu Lys Ala Ser Lys Met Val 130 135 140

Ser Val Glu Ser Val Leu Ala Ala Ala Arg Ile Ala Lys Asp Asn Gly 145 150 155 160

Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Asp Met Arg Gly Arg 165 170 175

Lys Thr Asn Leu Lys Asn Val Lys Thr Met Val Ser Glu Ile Arg Gly
180 185 190

Met Gly Met Glu Val Cys Val Thr Leu Gly Met Ile Asp Ala Glu Gln 195 200 205

Ala Gln Glu Leu Lys Glu Ala Gly Leu Thr Ala Tyr Asn His Asn Val 210 215 220

Asp Thr Ser Arg Asp Phe Tyr Pro Lys Val Ile Thr Thr Arg Thr Tyr 225 230 235 240

Asp Glu Arg Leu Asp Thr Ile Lys Asn Val Arg Glu Ala Gly Ile Asn 245 250 255

Val Cys Thr Gly Gly Ile Leu Gly Leu Gly Glu Asn Lys Ser Asp His 260 265 270

```
Ile Gly Leu Leu Glu Thr Val Ala Thr Leu Pro Ser His Pro Glu Ser
                          280
       275
Phe Pro Val Asn Met Leu Val Ala Ile Lys Gly Thr Pro Leu Glu Gly
                                         300
                      295
Asn Lys Lys Val Glu Phe Glu Asn Met Leu Arg Met Val Ala Thr Ala
                                     315
                                                        320
                  310
Arg Ile Val Met Pro Lys Thr Ile Val Arg Leu Ala Ala Gly Arg Gly
              325
                                 330
Glu Leu Ser Glu Glu Gln Gln Val Leu Cys Phe Met Ala Gly Ala Asn
                              345
Ala Val Phe Thr Gly Glu Thr Met Leu Thr Thr Pro Ala Val Gly Trp
Gly Val Asp Ser Val Val Phe Asn Arg Trp Gly Leu Arg Pro Met Glu
                      375
   370
Ser Phe Glu Val Glu Ala Leu Lys Asn Asp Lys Pro Ala Thr Thr Asn
                  390
                                     395
Thr Glu Ile Pro Val Glu Ala Ser Lys Ala Glu Met Pro Gly Thr Val
                                 410
              405
Ala
<210> 31
<211> 1032
<212> DNA
<213> Triticum aestivum
<400> 31
gcacgagaga tgccgtccta gaagcagcaa aaaaggcaaa ggaggctggg agcacccgat
tttgcatggg agccgcatgg agagagacaa ttggcaggaa aacaaatttc aaccagattc
                                                              120
ttgaatatgt caaggacata agaggtatgg gcatggaggt ctgttgcacc ctgggcatgc
tagagaaaca acaagctgaa gaactcaaga aggctggact tacagcttat aatcataacc
tagatacatc aagagaatat taccccaaca ttatttctac aagatcgtac gatgatagat
tacagactet teageatgte egtgaagetg gaataagegt etgeteaggt ggaattattg
gtcttggaga ggcggaggaa gaccgtgtag ggctgttgca tacactggcc actttgccaa
                                                              420
cacacccaga gagegttect atcaatgcat tgattgetgt caaaggcacg cetetteagg
atcagaagcc tgtagagata tgggaaatga tccgcatgat tgccagcgca cggattgtga
tgccaaaggc aatggtgaga ctttcggcag ggagagtacg gttttccatg ccagaacaag 600
ctctctgctt tctcgctggg gccaactcga tcttcgccgg tgaaaagctc ctgacaactg
cqaacaatga ctttgatgcg gaccaggcaa tgttcaagat ccttggcctg attcccaagg
                                                              720
ctccaaactt tggcgatgaa gaggtcatgg tagcagcacc cacggagaga tgtgagcaag
ccgctttgat gtaaaatgtc ggtatagatt ctcgagacca catccggtgc aaaactggca 840
ccattatctc cacctagagt tttgtactgt agagatcatg acattttata gtaacttcag
                                                              900
1032
aaaaaaaaa aa
<210> 32
```

<211> 263

<212> PRT

<213> Triticum aestivum

<400> 32
Thr Arg Asp Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ala Gly
1 5 10 15

Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg
20 25 30

Lys Thr Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg Gly 35 40 45

Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln Gln 50 60

Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu 65 70 75 80

Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Ser Thr Arg Ser Tyr 85 90 95

Asp Asp Arg Leu Gln Thr Leu Gln His Val Arg Glu Ala Gly Ile Ser 100 105 110

Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg 115 120 125

Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser 130 135 140

Val Pro Ile Asn Ala Leu Ile Ala Val Lys Gly Thr Pro Leu Gln Asp 145 150 155 160

Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Ser Ala 165 170 175

Arg Ile Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val 180 185 190

Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn 195 200 205

Ser Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe 210 215 220

Asp Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala 225 230 235 240

Pro Asn Phe Gly Asp Glu Glu Val Met Val Ala Ala Pro Thr Glu Arg 245 250 255

Cys Glu Gln Ala Ala Leu Met 260

<210> 33

<211> 378

<212> PRT

<213> Arabidopsis thaliana

<400> 33

Met Met Leu Val Arg Ser Val Phe Arg Ser Gln Leu Arg Pro Ser Val 1 5 10 15

- Ser Gly Gly Leu Gln Ser Ala Ser Cys Tyr Ser Ser Leu Ser Ala Ala 20 25 30
- Ser Ala Glu Ala Glu Arg Thr Ile Arg Glu Gly Pro Arg Asn Asp Trp 35 40 45
- Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Leu Leu Asp Leu 50 55 60
- Leu Phe His Gly Ala Gln Val His Arg His Val His Asn Phe Arg Glu 65 70 75 80
- Val Gln Gln Cys Thr Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu 85 90 95
- Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Ser Thr Gly Val Lys
 100 105 110
- Ala Gln Arg Leu Met Ser Lys Asp Ala Val Ile Asp Ala Ala Lys Lys 115 120 125
- Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg 130 135 140
- Asp Thr Ile Gly Arg Lys Thr Asn Phe Ser Gln Ile Leu Glu Tyr Ile 145 150 155 160
- Lys Glu Ile Arg Gly Met Gly Met Glu Val Cys Cys Thr Leu Gly Met 165 170 175
- Ile Glu Lys Gln Gln Ala Leu Glu Leu Lys Lys Ala Gly Leu Thr Ala 180 185 190
- Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Val Ile 195 200 205
- Thr Thr Arg Ser Tyr Asp Asp Arg Leu Glu Thr Leu Ser His Val Arg
- Asp Ala Gly Ile Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu 225 230 235 240
- Ala Glu Glu Asp Arg Ile Gly Leu Leu His Thr Leu Ala Thr Leu Pro 245 250 255
- Ser His Pro Glu Ser Val Pro Ile Asn Ala Leu Leu Ala Val Lys Gly 260 265 270
- Thr Pro Leu Glu Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg 275 280 285
- Met Ile Gly Thr Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu 290 295 300
- Ser Ala Gly Arg Val Arg Phe Ser Met Ser Glu Gln Ala Leu Cys Phe 305 310 315 320
- Leu Ala Gly Ala Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr
 325 330 335

Pro Asn Asn Asp Phe Asp Ala Asp Gln Leu Met Phe Lys Thr Leu Gly 340 345 350

Leu Ile Pro Lys Pro Pro Ser Phe Ser Glu Asp Asp Ser Glu Ser Glu 355 360 365

Asn Cys Glu Lys Val Ala Ser Ala Ser His 370 375

<210> 34

<211> 363

<212> PRT

<213> Schizosaccharomyces pombe

<400> 34

Met Phe Thr Arg Thr Ile Arg Gln Gln Ile Arg Arg Ser Ser Ala Leu
1 5 10 15

Ser Leu Val Arg Asn Asn Trp Thr Arg Glu Glu Ile Gln Lys Ile Tyr 20 25 30

Asp Thr Pro Leu Ile Asp Leu Ile Phe Arg Ala Ala Ser Ile His Arg 35 40 45

Lys Phe His Asp Pro Lys Lys Val Gln Gln Cys Thr Leu Leu Ser Ile 50 55 60

Lys Thr Gly Gly Cys Thr Glu Asp Cys Lys Tyr Cys Ala Gln Ser Ser 65 70 75 80

Arg Tyr Asn Thr Gly Val Lys Ala Thr Lys Leu Met Lys Ile Asp Glu 85 90 95

Val Leu Glu Lys Ala Lys Ile Ala Lys Ala Lys Gly Ser Thr Arg Phe 100 105 110

Cys Met Gly Ser Ala Trp Arg Asp Leu Asn Gly Arg Asn Arg Thr Phe 115 120 125

Lys Asn Ile Leu Glu Ile Ile Lys Glu Val Arg Ser Met Asp Met Glu 130 135 140

Val Cys Val Thr Leu Gly Met Leu Asn Glu Gln Gln Ala Lys Glu Leu 145 150 155 160

Lys Asp Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr Ser Arg 165 170 175

Glu Tyr Tyr Ser Lys Ile Ile Ser Thr Arg Thr Tyr Asp Glu Arg Leu 180 185 190

Asn Thr Ile Asp Asn Leu Arg Lys Ala Gly Leu Lys Val Cys Ser Gly
195 200 205

Gly Ile Leu Gly Leu Gly Glu Lys Lys His Asp Arg Val Gly Leu Ile 210 215 220

His Ser Leu Ala Thr Met Pro Thr His Pro Glu Ser Val Pro Phe Asn 225 230 235 240

Leu Leu Val Pro Ile Pro Gly Thr Pro Val Gly Asp Ala Val Lys Glu 245 250 255

Arg Leu Pro Ile His Pro Phe Leu Arg Ser Ile Ala Thr Ala Arg Ile 260 265 270

Cys Met Pro Lys Thr Ile Ile Arg Phe Ala Ala Gly Arg Asn Thr Cys 275 280 285

Ser Glu Ser Glu Gln Ala Leu Ala Phe Met Ala Gly Ala Asn Ala Val 290 295 300

Phe Thr Gly Glu Lys Met Leu Thr Thr Pro Ala Val Ser Trp Asp Ser 305 310 315 320

Asp Ser Gln Leu Phe Tyr Asn Trp Gly Leu Glu Gly Met Gln Ser Phe 325 330 335

Glu Tyr Gly Thr Ser Thr Glu Gly Glu Asp Gly Thr Phe Thr Leu Pro 340 345 350

Pro Lys Glu Arg Leu Ala Pro Ser Pro Ser Leu 355 360

<210> 35

<211> 375

<212> PRT

<213> Saccharomyces cerevisiae

<400> 35

Met Met Ser Thr Ile Tyr Arg His Leu Ser Thr Ala Arg Pro Ala Leu 1 5 10 15

Thr Lys Tyr Ala Thr Asn Ala Ala Val Lys Ser Thr Thr Ala Ser Ser 20 25 30

Glu Ala Ser Thr Leu Gly Ala Leu Gln Tyr Ala Leu Ser Leu Asp Glu 35 40 45

Pro Ser His Ser Trp Thr Lys Ser Gln Leu Lys Glu Ile Tyr His Thr 50 55 60

Pro Leu Leu Glu Leu Thr His Ala Ala Gln Leu Gln His Arg Lys Trp 65 70 75 80

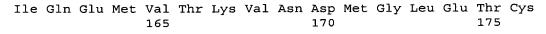
His Asp Pro Thr Lys Val Gln Leu Cys Thr Leu Met Asn Ile Lys Ser 85 90 95

Gly Gly Cys Ser Glu Asp Cys Lys Tyr Cys Ala Gln Ser Ser Arg Asn 100 105 110

Asp Thr Gly Leu Lys Ala Glu Lys Met Val Lys Val Asp Glu Val Ile 115 120 125

Lys Glu Ala Glu Glu Ala Lys Arg Asn Gly Ser Thr Arg Phe Cys Leu 130 135 140

Gly Ala Ala Trp Arg Asp Met Lys Gly Arg Lys Ser Ala Met Lys Arg 145 150 155 160



Val Thr Leu Gly Met Val Asp Gln Asp Gln Ala Lys Gln Leu Lys Asp 180 185 190

Ala Gly Leu Thr Ala Tyr Asn His Asn Ile Asp Thr Ser Arg Glu His
195 200 205

Tyr Ser Lys Val Ile Thr Thr Arg Thr Tyr Asp Asp Arg Leu Gln Thr 210 220

Ile Lys Asn Val Gln Glu Ser Gly Ile Lys Ala Cys Thr Gly Gly Ile 225 230 235 240

Leu Gly Leu Gly Glu Ser Glu Asp Asp His Ile Gly Phe Ile Tyr Thr 245 250 255

Leu Ser Asn Met Ser Pro His Pro Glu Ser Leu Pro Ile Asn Arg Leu 260 265 270

Val Ala Ile Lys Gly Thr Pro Met Ala Glu Glu Leu Ala Asp Pro Lys 275 280 285

Ser Lys Lys Leu Gln Phe Asp Glu Ile Leu Arg Thr Ile Ala Thr Ala 290 295 300

Arg Ile Val Met Pro Lys Ala Ile Ile Arg Leu Ala Ala Gly Arg Tyr 305 310 315 320

Thr Met Lys Glu Thr Glu Gln Phe Val Cys Phe Met Ala Gly Cys Asn
325 330 335

Ser Ile Phe Thr Gly Lys Lys Met Leu Thr Thr Met Cys Asn Gly Trp 340 345 350

Asp Glu Asp Lys Ala Met Leu Ala Lys Trp Gly Leu Gln Pro Met Glu 355 360 365

Ala Phe Lys Tyr Asp Arg Ser

<210> 36

<211> 12

<212> PRT

<213>

<400> 36

Gly Xaa Cys Xaa Glu Asp Cys Xaa Tyr Cys Xaa Gln